**Highly variable microbiota development in the chicken gastrointestinal tract: are hygiene levels to blame?**

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**Supplementary Figure**

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**Figure S1:** Boxplots of the OTUs most differentially abundant (p<10-10) between the 3 trials, generated using R phylogenetic package ade4 and Qiime analysis outputs. The p-values are calculated using Qiime ANOVA. For OTUs with similarity to closest type strain in EzTaxon database > 95%, taxonomy is given as EzTaxon strain and similarity, for OTUs with lower similarity taxonomy is given at an order level.